GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 17:25:17 ; Search time 4674.33 Seconds
                                           (without alignments)
                                           16997.243 Million cell updates/sec

Title: US-09-596-194-59
Perfect score: 2730
Sequence: 1 gtcgacccacgcgtccgtcc..........aaaaaaaaaagggcggccgc 2730

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1:   gb_ba:*
                2:   gb_htg:*
                3:   gb_in:*
                4:   gb_om:*
                5:   gb_ov:*
                6:   gb_pat:*
                7:   gb_ph:*
                8:   gb_pl:*
                9:   gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
                15: em_ba:*
                16: em_fun:*
                17: em_hum:*
                18: em_in:*
                19: em_mu:*
                20: em_om:*
                21: em_or:*
                22: em_ov:*
                23: em_pat:*
                24: em_ph:*
                25: em_pl:*
                26: em_ro:*
                27: em_sts:*

[handwritten] repeated in:
Gen Seq
US Pats
US PG PUBS
EST

```
                     GenCore version 5.1.4_p5_4578
              Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:           June  1, 2003, 17:25:17 ; Search time 3446.67 Seconds
                                           (without alignments)
                                           16997.243 Million cell updates/sec


Title:            US-09-596-194-60
Perfect score:    2013
Sequence:         1 atggcccagctgttcctgcc..........ccctgcagctctgggtcacc 2013

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:       4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
                  1:  gb_ba:*
                  2:  gb_htg:*
                  3:  gb_in:*
                  4:  gb_om:*
                  5:  gb_ov:*
                  6:  gb_pat:*
                  7:  gb_ph:*
                  8:  gb_pl:*
                  9:  gb_pr:*
                  10:  gb_ro:*
                  11:  gb_sts:*
                  12:  gb_sy:*
                  13:  gb_un:*
                  14:  gb_vi:*
                  15:  em_ba:*
                  16:  em_fun:*
                  17:  em_hum:*
                  18:  em_in:*
                  19:  em_mu:*
                  20:  em_om:*
                  21:  em_or:*
                  22:  em_ov:*
                  23:  em_pat:*
                  24:  em_ph:*
                  25:  em_pl:*
                  26:  em_ro:*
                  27:  em_sts:*
                  28:  em_un:*
```

Search repeated in
Gen Seq
US Pats
US PG Pubs
EST

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 12:47:26 ; Search time 3221.31 Seconds
                                           (without alignments)
                                           6062.128 Million cell updates/sec

Title: US-09-596-194-61
Perfect score: 671
Sequence: 1 MAQLFLPLLAALVLAQAPAA.........QGSTALSILLLFFPLQLWVT 671

Scoring table: OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 200

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09596194/runat_27052003_102512_11306/app_query.fasta_1.1
678
-DB=GenEmbl -QFMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=200 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09596194_@CGN_1_1_4069_@runat_27052003_102512_11306 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*   —   _Search also run in_
                 1: gb_ba:*
                 2: gb_htg:*   _US Pats_
                 3: gb_in:*
                 4: gb_om:*   _Gen Seq_
                 5: gb_ov:*
                 6: gb_pat:*   _US PGPubs_
                 7: gb_ph:*
                 8: gb_pl:*   _EST_
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 12:47:26 ; Search time 3115.69 Seconds
                                          (without alignments)
                                          6062.128 Million cell updates/sec

Title: US-09-596-194-63
Perfect score: 649
Sequence: 1 DVLEGDSSEDRAFRVRIAGD..........QGSTALSILLLFFPLQLWVT 649

Scoring table: OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 200

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09596194/runat_27052003_102512_11306/app_query.fasta_1.1
678
-DB=GenEmbl -QFMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=200 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09596194_@CGN_1_1_4069_@runat_27052003_102512_11306 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*

Identical search repeated in
GenSeq
US Pats
US PGPUbs
EST

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 08:42:01 ; Search time 3213.17 Seconds
                                             (without alignments)
                                             6077.472 Million cell updates/sec

Title: US-09-596-194-61
Perfect score: 3492
Sequence: 1 MAQLFLPLLAALVLAQAPAA.........QGSTALSILLLFFPLQLWVT 671

Scoring table: BLOSUM62
                    Xgapop 10.0 , Xgapext   0.5
                    Ygapop 10.0 , Ygapext   0.5
                    Fgapop 6.0 , Fgapext   7.0
                    Delop   6.0 , Delext   7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09596194/runat_27052003_102430_10900/app_query.fasta_1.1
678
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09596194_@CGN_1_1_4069_@runat_27052003_102430_10900 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                    Identical search repeated in GENSEQ, US Patents, US PGPUBS, EST
databases

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 08:42:01 ; Search time 3107.82 Seconds
                                            (without alignments)
                                            6077.472 Million cell updates/sec

Title: US-09-596-194-63
Perfect score: 3393
Sequence: 1 DVLEGDSSEDRAFRVRIAGD..........QGSTALSILLLFFPLQLWVT 649

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext   0.5
                  Ygapop 10.0 , Ygapext   0.5
                  Fgapop 6.0 , Fgapext   7.0
                  Delop   6.0 , Delext   7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09596194/runat_27052003_102430_10900/app_query.fasta_1.1
678
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09596194_@CGN_1_1_4069_@runat_27052003_102430_10900 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
Identical search repeated in GENSEQ, US Patents, US PGPUBS, EST databases